117. (New) The method of claim 116, wherein the DNA molecules are obtained from uncultivated organisms in the environmental source.

118. (New) The method of claim 117, wherein introduction of the at least one mutation comprises directed evolution mutagenesis.

119. (New) The method of claim 116, ~~further comprising~~ the step of: expressing the mutagenized molecule of step (b) to create a bioactivity or biomolecule containing a mutation.

120. (New) The method of claim 116, wherein the DNA molecules are genomic DNA.

121. (New) The method of claim 120, wherein the genomic DNA is at least 1 Kb in size.

122. (New) The method of claim 120, wherein the genomic DNA is at least 5 Kb in size.

123. (New) The method of claim 120, wherein the genomic DNA is at least 10 Kb in size.

124. (New) The method of claim 120, wherein the genomic DNA is at least 15 Kb in size.

125. (New) The method of claim 120, wherein the genomic DNA is at least 20 Kb in size.

126. (New) The method of claim 120, wherein the genomic DNA is at least 25 Kb in size.

127. (New) The method of claim 120, wherein the genomic DNA is at least 30 Kb in size.

128. (New) The method of claim 120, wherein the genomic DNA is at least 40 Kb in size.

129. (New) The method of claim 120, wherein the genomic DNA is at least 60 Kb in size.

130. (New) The method of claim 120, wherein the genomic DNA is at least 100 Kb in size.

131. (New) The method of claim 120, wherein the genomic DNA is at least 200 Kb in size.

132. (New) The method of claim 116, wherein the mutagenized DNA molecule includes a gene cluster.

133. (New) The method of claim 116, wherein the mutagenized DNA comprises one or more operons, or portions thereof.

134. (New) The method of claim 133, wherein the operon, or portions thereof, encodes a complete or partial metabolic pathway.

135. (New) The method of claim 133, wherein the operon produces a molecule selected from a polyketide synthase, a polyketides, an anti-cancer agent, and an imunosuppressant.

136. (New) The method of claim 116, wherein the molecule is suitable for veterinary use.

137. (New) The method of claim 116, ~~wherein the~~ DNA molecules are inserted into a vector prior to step a).

138. (New) The method of claim 137, wherein the vector is selected from viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, and viral DNA.

139. (New) The method of claim 116, wherein the environmental sample is selected from, soil, water, permafrost, materials of volcanic origin, and plants.

140. (New) The method of claim 139, wherein the environmental sample is obtained from Arctic, Antarctic or tropical areas.

141. (New) The method of claim 116, wherein the DNA molecules obtained in step a) are enriching for a particular organism or organisms of interest.

142. (New) The method of claim 116 where the DNA molecules are derived from a plurality of donor organisms.

143. (New) The method of claim 116, where the screening comprises activity or hybridization screening.

144. (New) A method for generating a protein with an improved activity of interest, said method comprising:

a) selecting a wild-type DNA sequence from a library of DNA sequences isolated from a heterogeneous population of microorganisms;

b) introducing a mutation into the selected wild-type DNA sequence to form a mutated DNA sequence; and

c) determining whether a protein encoded by the mutated DNA sequence provides an improved activity of interest in comparison to a protein encoded by the wild-type DNA sequence.

145. (New) The method of claim 144, wherein the library of DNA sequences is a library of cDNA sequences.

146. (New) The method of claim 144, wherein the mutation is introduced by a method selected from error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis and site-specific mutagenesis.

147. (New) The method of claim 144, comprising screening the library for an additional DNA sequence that provides the activity of interest, prior to introducing a mutation into the wild-type DNA sequence.

148. (New) The method of claim 144, wherein the improved activity of interest comprises an improved enzymatic activity.

149. (New) The method of claim 144, wherein the selection of the wild-type DNA sequence comprises contacting the wild-type sequence with a complementary nucleic acid.

150. (New) The method of claim 149, wherein the complementary nucleic acid comprises a hybridization probe bound to a solid phase.

151. (New) The method of claim 144, wherein the microorganisms comprise prokaryotes.

152. (New) The method of claim 151, wherein the prokaryotes comprise microorganisms selected from Eubacteria and Archbacteria.

153. (New) The method of claim 144, wherein the microorganisms comprise eukaryotes.

154. (New) The method of claim 153, wherein the eukaryotes comprise microorganisms selected from fungi, algae and protozoa.

155. (New) The method of claim 144, wherein the microorganisms comprise extremeophiles.

156. (New) The method of claim 155, wherein the extremeophiles comprise organisms selected from thermophiles, hyperthermophiles, psychrophiles and psychrotropes.

157. (New) A method for enhancing the activity of a protein encoded by a nucleotide sequence, said method comprising:

(a) isolating at least two gene sequences encoding enzymes having a common characteristic from a library of gene sequences, wherein the library of gene sequences is derived from a heterogeneous population of microorganisms;

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(b) mutating the gene sequences selected in (a); and

(c) screening the mutated gene sequences to identify a gene sequence that encodes a protein having an enhanced activity of interest.

158. (New) The method of claim 157, wherein mutating the gene sequences comprises a method selected from error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis and site- specific mutagenesis.

159. (New) The method of claim 157, wherein the library of gene sequences comprises cDNA sequences.

160. (New) The method of claim 157, wherein the microorganisms comprise prokaryotes.

161. (New) The method of claim 160, wherein the prokaryotes comprise microorganisms selected from Eubacteria and Archaebacteria.

162. (New) The method of claim 157, wherein the microorganisms comprise eukaryotes.

163. (New) The method of claim 162, wherein the eukaryotes comprise microorganisms selected from fungi, algae and protozoa.

164. (New) The method of claim 157, wherein the microorganisms comprise extremeophiles.

165. (New) The method of claim 164, wherein the extremeophiles are selected from thermophiles, hyperthermophiles, psychrophiles and psychrotropes.

166. (New) The method of claim 157, wherein the improved activity is an enzymatic activity.--